T. Haas   **RECEIVED**   #13

AUG 08 2000

TECH CENTER 1600/2900

1638

ENTERED

```
RAW SEQUENCE LISTING                    DATE: 07/27/2000
PATENT APPLICATION:  US/08/945,144      TIME: 12:59:09

Input Set : A:\Rpmu5e.app
Output Set: N:\CRF3\07272000\H945144.raw
```

```
      3 <110> APPLICANT: Lebrun, Michel
      4        Sailland, Alain
      5        Freyssinet, Georges
      6        DeGryse, Eric
      8 <120> TITLE OF INVENTION: Mutated 5-Enol Pyruvylshikimate-3-Phosphate Synthase,
      9        Gene Coding for Said Protein and Transformed Plants
     10        Containing Said Gene
     12 <130> FILE REFERENCE: 5500-13
     14 <140> CURRENT APPLICATION NUMBER: 08/945,144
C--> 15 <141> CURRENT FILING DATE: 1998-12-01
     17 <150> PRIOR APPLICATION NUMBER: PCT/FR96/01125
     18 <151> PRIOR FILING DATE: 1996-07-18
     20 <150> PRIOR APPLICATION NUMBER: FRANCE 95/08979
     21 <151> PRIOR FILING DATE: 1995-07-19
     23 <160> NUMBER OF SEQ ID NOS: 5
     25 <170> SOFTWARE: PatentIn Ver. 2.0
     27 <210> SEQ ID NO: 1
     28 <211> LENGTH: 1713
     29 <212> TYPE: DNA
     30 <213> ORGANISM: Zea mays
     32 <400> SEQUENCE: 1
     33 aatcaatttc acacaggaaa cagctatgac catgattacg aattcgggcc cgggcgcgtg 60
     35 atccggcggc ggcagcggcg gcggcggttgc aggcgggtgc cgaggagatc gtgctgcagc 120
     37 ccatcaagga gatctccggc accgtcaagc tgccggggtc caagtcgctt tccaaccgga 180
     39 tcctcctact cgccgccctg tccgagggga caacagtggt tgataacctg ctgaacagtg 240
     41 aggatgtcca ctacatgctc ggggccttga ggactcttgg tctctctgtc gaagcggaca 300
     43 aagctgccaa aagagctgta gttgttggct gtggtggaaa gttcccagtt gaggatgcta 360
     45 aagaggaagt gcagctcttc ttggggaatg ctggaactgc aatgcggcca ttgacagcag 420
     47 ctgttactgc tgctggtgga aatgcaactt acgtgcttga tggagtacca agaatgaggg 480
     49 agagaccat tggcgacttg gttgtcggat tgaagcagct tggtgcagat gttgattgtt 540
     51 tccttggcac tgactgccca cctgttcgtg tcaatgaat cggagggcta cctggtggca 600
     53 aggtcaagct gtctggctcc atcagcagtc agtacttgag tgccttgctg atggctgctc 660
     55 ctttggctct tggggatgtg gagattgaaa tcattgataa attaatctcc attccgtacg 720
     57 tcgaaatgac attgagattg atggagcgtt ttggtgtgaa agcagagcat tctgatagct 780
     59 gggacagatt ctacattaag ggaggtcaaa aatacaagtc ccctaaaaat gcctatgttg 840
     61 aaggtgatgc ctcaagcgca agctatttct tggctggtgc tgcaattact ggagggactg 900
     63 tgactgtgga aggttgtggc accaccagtt tgcagggtga tgtgaagttt gctgaggtac 960
     65 tggagatgat gggagcgaag gttacatgga ccgagactag cgtaactgtt actggcccac 1020
     67 cgcgggagcc atttgggagg aaacacctca aggcgattga tgtcaacatg aacaagatgc 1080
     69 ctgatgtcgc catgactctt gctgtggttg ccctctttgc cgatggcccg acagccatca 1140
     71 gagacgtggc ttcctggaga gtaaaggaga ccgagaggat ggttgcgatc cggacggagc 1200
     73 taaccaagct gggagcatct gttgaggaag ggccggacta ctgcatcatc acgccgccgg 1260
     75 agaagctgaa cgtgacggcg atcgacacgt acgacgacca caggatggcc atggccttct 1320
     77 cccttgccgc ctgtgccgag gtccccgtca ccatccggga ccctgggtgc acccggaaga 1380
     79 ccttcccga ctacttcgat gtgctgagca ctttcgtcaa gaattaataa agcgtgcgat 1440
     81 actaccacgc agcttgattg aagtgatagg cttgtgctga ggaaatacat ttctttgtt 1500
     83 ctgtttttct ctttcacggg attaagtttt gagtctgtaa cgttagttgt ttgtagcaag 1560
```

```
85 tttctatttc ggatcttaag tttgtgcact gtaagccaaa tttcatttca agagtggttc 1620
87 gttggaataa taagaataat aaattacgtt tcagtgaaaa aaaaaaaaaa aaaaaaaaaa 1680
89 aaaaaaaaaa aaaaaaaaaa aacccgggaa ttc                             1713
92 <210> SEQ ID NO: 2
93 <211> LENGTH: 1340
94 <212> TYPE: DNA
95 <213> ORGANISM: Zea mays
97 <220> FEATURE:
98 <221> NAME/KEY: CDS
99 <222> LOCATION: (6)..(1337)
101 <400> SEQUENCE: 2
102 ccatg gcc ggc gcc gag gag atc gtg ctg cag ccc atc aag gag atc tcc  50
103       Ala Gly Ala Glu Glu Ile Val Leu Gln Pro Ile Lys Glu Ile Ser
104        1               5                  10                  15
106 ggc acc gtc aag ctg ccg ggg tcc aag tcg ctt tcc aac cgg atc ctc   98
107 Gly Thr Val Lys Leu Pro Gly Ser Lys Ser Leu Ser Asn Arg Ile Leu
108              20                  25                  30
110 cta ctc gcc gcc ctg tcc gag ggg aca aca gtg gtt gat aac ctg ctg  146
111 Leu Leu Ala Ala Leu Ser Glu Gly Thr Thr Val Val Asp Asn Leu Leu
112          35                  40                  45
114 aac agt gag gat gtc cac tac atg ctc ggg gcc ttg agg act ctt ggt  194
115 Asn Ser Glu Asp Val His Tyr Met Leu Gly Ala Leu Arg Thr Leu Gly
116          50                  55                  60
118 ctc tct gtc gaa gcg gac aaa gct gcc aaa aga gct gta gtt gtt ggc  242
119 Leu Ser Val Glu Ala Asp Lys Ala Ala Lys Arg Ala Val Val Val Gly
120      65                  70                  75
122 tgt ggt gga aag ttc cca gtt gag gat gct aaa gag gaa gtg cag ctc  290
123 Cys Gly Gly Lys Phe Pro Val Glu Asp Ala Lys Glu Glu Val Gln Leu
124  80                  85                  90                  95
126 ttc ttg ggg aat gct gga act gca atg cgg cca ttg aca gca gct gtt  338
127 Phe Leu Gly Asn Ala Gly Thr Ala Met Arg Pro Leu Thr Ala Ala Val
128              100                 105                 110
130 act gct gct ggt gga aat gca act tac gtg ctt gat gga gta cca aga  386
131 Thr Ala Ala Gly Gly Asn Ala Thr Tyr Val Leu Asp Gly Val Pro Arg
132          115                 120                 125
134 atg agg gag aga ccc att ggc gac ttg gtt gtc gga ttg aag cag ctt  434
135 Met Arg Glu Arg Pro Ile Gly Asp Leu Val Val Gly Leu Lys Gln Leu
136          130                 135                 140
138 ggt gca gat gtt gat tgt ttc ctt ggc act gac tgc cca cct gtt cgt  482
139 Gly Ala Asp Val Asp Cys Phe Leu Gly Thr Asp Cys Pro Pro Val Arg
140      145                 150                 155
142 gtc aat gga atc gga ggg cta cct ggt ggc aag gtc aag ctg tct ggc  530
143 Val Asn Gly Ile Gly Gly Leu Pro Gly Gly Lys Val Lys Leu Ser Gly
144 160                 165                 170                 175
146 tcc atc agc agt cag tac ttg agt gcc ttg ctg atg gct gct cct ttg  578
147 Ser Ile Ser Ser Gln Tyr Leu Ser Ala Leu Leu Met Ala Ala Pro Leu
148              180                 185                 190
150 gct ctt ggg gat gtg gag att gaa atc att gat aaa tta atc tcc att  626
151 Ala Leu Gly Asp Val Glu Ile Glu Ile Ile Asp Lys Leu Ile Ser Ile
```

```
                RAW SEQUENCE LISTING                   DATE: 07/27/2000
                PATENT APPLICATION:  US/08/945,144     TIME: 12:59:09

                Input Set : A:\Rpmu5e.app
                Output Set: N:\CRF3\07272000\H945144.raw

152                195                 200                 205
154 ccg tac gtc gaa atg aca ttg aga ttg atg gag cgt ttt ggt gtg aaa    674
155 Pro Tyr Val Glu Met Thr Leu Arg Leu Met Glu Arg Phe Gly Val Lys
156         210                 215                 220
158 gca gag cat tct gat agc tgg gac aga ttc tac att aag gga ggt caa    722
159 Ala Glu His Ser Asp Ser Trp Asp Arg Phe Tyr Ile Lys Gly Gly Gln
160     225                 230                 235
162 aaa tac aag tcc cct aaa aat gcc tat gtt gaa ggt gat gcc tca agc    770
163 Lys Tyr Lys Ser Pro Lys Asn Ala Tyr Val Glu Gly Asp Ala Ser Ser
164 240                 245                 250                 255
166 gca agc tat ttc ttg gct ggt gct gca att act gga ggg act gtg act    818
167 Ala Ser Tyr Phe Leu Ala Gly Ala Ala Ile Thr Gly Gly Thr Val Thr
168             260                 265                 270
170 gtg gaa ggt tgt ggc acc acc agt ttg cag ggt gat gtg aag ttt gct    866
171 Val Glu Gly Cys Gly Thr Thr Ser Leu Gln Gly Asp Val Lys Phe Ala
172             275                 280                 285
174 gag gta ctg gag atg atg gga gcg aag gtt aca tgg acc gag act agc    914
175 Glu Val Leu Glu Met Met Gly Ala Lys Val Thr Trp Thr Glu Thr Ser
176         290                 295                 300
178 gta act gtt act ggc cca ccg cgg gag cca ttt ggg agg aaa cac ctc    962
179 Val Thr Val Thr Gly Pro Pro Arg Glu Pro Phe Gly Arg Lys His Leu
180     305                 310                 315
182 aag gcg att gat gtc aac atg aac aag atg cct gat gtc gcc atg act    1010
183 Lys Ala Ile Asp Val Asn Met Asn Lys Met Pro Asp Val Ala Met Thr
184 320                 325                 330                 335
186 ctt gct gtg gtt gcc ctc ttt gcc gat ggc aca gcc atc aga gac    1058
187 Leu Ala Val Val Ala Leu Phe Ala Asp Gly Pro Thr Ala Ile Arg Asp
188             340                 345                 350
190 gtg gct tcc tgg aga gta aag gag acc gag agg atg gtt gcg atc cgg    1106
191 Val Ala Ser Trp Arg Val Lys Glu Thr Glu Arg Met Val Ala Ile Arg
192             355                 360                 365
194 acg gag cta acc aag ctg gga gca tct gtt gag gaa ggg ccg gac tac    1154
195 Thr Glu Leu Thr Lys Leu Gly Ala Ser Val Glu Glu Gly Pro Asp Tyr
196         370                 375                 380
198 tgc atc atc acg ccg ccg gag aag ctg aac gtg acg gcg atc gac acg    1202
199 Cys Ile Ile Thr Pro Pro Glu Lys Leu Asn Val Thr Ala Ile Asp Thr
200     385                 390                 395
202 tac gac gac cac agg atg gcc atg gcc ttc tcc ctt gcc gcc tgt gcc    1250
203 Tyr Asp Asp His Arg Met Ala Met Ala Phe Ser Leu Ala Ala Cys Ala
204 400                 405                 410                 415
206 gag gtc ccc gtc acc atc cgg gac cct ggg tgc acc cgg aag acc ttc    1298
207 Glu Val Pro Val Thr Ile Arg Asp Pro Gly Cys Thr Arg Lys Thr Phe
208             420                 425                 430
210 ccc gac tac ttc gat gtg ctg agc act ttc gtc aag aat taa    1340
211 Pro Asp Tyr Phe Asp Val Leu Ser Thr Phe Val Lys Asn
212             435                 440
215 <210> SEQ ID NO: 3
216 <211> LENGTH: 444
217 <212> TYPE: PRT
```

Input Set : A:\Rpmu5e.app
Output Set: N:\CRF3\07272000\H945144.raw

```
218 <213> ORGANISM: Zea mays
220 <400> SEQUENCE: 3
221 Ala Gly Ala Glu Glu Ile Val Leu Gln Pro Ile Lys Glu Ile Ser Gly
222  1               5                  10                  15
224 Thr Val Lys Leu Pro Gly Ser Lys Ser Leu Ser Asn Arg Ile Leu Leu
225            20                  25                  30
227 Leu Ala Ala Leu Ser Glu Gly Thr Thr Val Val Asp Asn Leu Leu Asn
228            35                  40                  45
230 Ser Glu Asp Val His Tyr Met Leu Gly Ala Leu Arg Thr Leu Gly Leu
231        50                  55                  60
233 Ser Val Glu Ala Asp Lys Ala Ala Lys Arg Ala Val Val Val Gly Cys
234  65                  70                  75                  80
236 Gly Gly Lys Phe Pro Val Glu Asp Ala Lys Glu Glu Val Gln Leu Phe
237            85                  90                  95
239 Leu Gly Asn Ala Gly Thr Ala Met Arg Pro Leu Thr Ala Ala Val Thr
240            100                 105                 110
242 Ala Ala Gly Gly Asn Ala Thr Tyr Val Leu Asp Gly Val Pro Arg Met
243            115                 120                 125
245 Arg Glu Arg Pro Ile Gly Asp Leu Val Val Gly Leu Lys Gln Leu Gly
246        130                 135                 140
248 Ala Asp Val Asp Cys Phe Leu Gly Thr Asp Cys Pro Pro Val Arg Val
249 145                 150                 155                 160
251 Asn Gly Ile Gly Gly Leu Pro Gly Gly Lys Val Lys Leu Ser Gly Ser
252            165                 170                 175
254 Ile Ser Ser Gln Tyr Leu Ser Ala Leu Leu Met Ala Ala Pro Leu Ala
255            180                 185                 190
257 Leu Gly Asp Val Glu Ile Glu Ile Ile Asp Lys Leu Ile Ser Ile Pro
258        195                 200                 205
260 Tyr Val Glu Met Thr Leu Arg Leu Met Glu Arg Phe Gly Val Lys Ala
261        210                 215                 220
263 Glu His Ser Asp Ser Trp Asp Arg Phe Tyr Ile Lys Gly Gly Gln Lys
264 225                 230                 235                 240
266 Tyr Lys Ser Pro Lys Asn Ala Tyr Val Glu Gly Asp Ala Ser Ser Ala
267            245                 250                 255
269 Ser Tyr Phe Leu Ala Gly Ala Ala Ile Thr Gly Gly Thr Val Thr Val
270            260                 265                 270
272 Glu Gly Cys Gly Thr Thr Ser Leu Gln Gly Asp Val Lys Phe Ala Glu
273        275                 280                 285
275 Val Leu Glu Met Met Gly Ala Lys Val Thr Trp Thr Glu Thr Ser Val
276        290                 295                 300
278 Thr Val Thr Gly Pro Pro Arg Glu Pro Phe Gly Arg Lys His Leu Lys
279 305                 310                 315                 320
281 Ala Ile Asp Val Asn Met Asn Lys Met Pro Asp Val Ala Met Thr Leu
282            325                 330                 335
284 Ala Val Val Ala Leu Phe Ala Asp Gly Pro Thr Ala Ile Arg Asp Val
285            340                 345                 350
287 Ala Ser Trp Arg Val Lys Glu Thr Glu Arg Met Val Ala Ile Arg Thr
288        355                 360                 365
290 Glu Leu Thr Lys Leu Gly Ala Ser Val Glu Glu Gly Pro Asp Tyr Cys
```

Input Set : A:\Rpmu5e.app
Output Set: N:\CRF3\07272000\H945144.raw

```
291     370                    375                     380
293 Ile Ile Thr Pro Pro Glu Lys Leu Asn Val Thr Ala Ile Asp Thr Tyr
294 385                     390                     395                 400
296 Asp Asp His Arg Met Ala Met Ala Phe Ser Leu Ala Ala Cys Ala Glu
297                  405                     410                     415
299 Val Pro Val Thr Ile Arg Asp Pro Gly Cys Thr Arg Lys Thr Phe Pro
300             420                     425                     430
302 Asp Tyr Phe Asp Val Leu Ser Thr Phe Val Lys Asn
303          435                     440
306 <210> SEQ ID NO: 4
307 <211> LENGTH: 1340
308 <212> TYPE: DNA
309 <213> ORGANISM: Zea mays
311 <220> FEATURE:
312 <221> NAME/KEY: CDS
313 <222> LOCATION: (6)..(1337)
315 <400> SEQUENCE: 4
316 ccatg gcc ggc gcc gag gag atc gtg ctg cag ccc atc aag gag atc tcc 50
317       Ala Gly Ala Glu Glu Ile Val Leu Gln Pro Ile Lys Glu Ile Ser
318        1               5                  10                  15
320 ggc acc gtc aag ctg ccg ggg tcc aag tcg ctt tcc aac cgg atc ctc   98
321 Gly Thr Val Lys Leu Pro Gly Ser Lys Ser Leu Ser Asn Arg Ile Leu
322                  20                  25                  30
324 cta ctc gcc gcc ctg tcc gag ggg aca aca gtg gtt gat aac ctg ctg  146
325 Leu Leu Ala Ala Leu Ser Glu Gly Thr Thr Val Val Asp Asn Leu Leu
326             35                  40                  45
328 aac agt gag gat gtc cac tac atg ctc ggg gcc ttg agg act ctt ggt  194
329 Asn Ser Glu Asp Val His Tyr Met Leu Gly Ala Leu Arg Thr Leu Gly
330          50                  55                  60
332 ctc tct gtc gaa gcg gac aaa gct gcc aaa aga gct gta gtt gtt ggc  242
333 Leu Ser Val Glu Ala Asp Lys Ala Ala Lys Arg Ala Val Val Val Gly
334       65                  70                  75
336 tgt ggt gga aag ttc cca gtt gag gat gct aaa gag gaa gtg cag ctc  290
337 Cys Gly Gly Lys Phe Pro Val Glu Asp Ala Lys Glu Glu Val Gln Leu
338  80                  85                  90                  95
340 ttc ttg ggg aat gct gga atc gca atg cgg tcc ttg aca gca gct gtt  338
341 Phe Leu Gly Asn Ala Gly Ile Ala Met Arg Ser Leu Thr Ala Ala Val
342             100                 105                 110
344 act gct gct ggt gga aat gca act tac gtg ctt gat gga gta cca aga  386
345 Thr Ala Ala Gly Gly Asn Ala Thr Tyr Val Leu Asp Gly Val Pro Arg
346             115                 120                 125
348 atg agg gag aga ccc att ggc gac ttg gtt gtc gga ttg aag cag ctt  434
349 Met Arg Glu Arg Pro Ile Gly Asp Leu Val Val Gly Leu Lys Gln Leu
350          130                 135                 140
352 ggt gca gat gtt gat tgt ttc ctt ggc act gac tgc cca cct gtt cgt  482
353 Gly Ala Asp Val Asp Cys Phe Leu Gly Thr Asp Cys Pro Pro Val Arg
354       145                 150                 155
356 gtc aat gga atc gga ggg cta cct ggt ggc aag gtc aag ctg tct ggc  530
357 Val Asn Gly Ile Gly Gly Leu Pro Gly Gly Lys Val Lys Leu Ser Gly
```

VERIFICATION SUMMARY   DATE: 07/27/2000
PATENT APPLICATION: US/08/945,144   TIME: 12:59:10

Input Set : A:\Rpmu5e.app
Output Set: N:\CRF3\07272000\H945144.raw

L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date